

SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd.

<120> Screening method of agents for increasing insulin content

<130> Y0352PCT-698

<150> JP 2002-265622

<151> 2002-09-11

<150> JP 2003-056813

<151> 2003-03-04

<160> 7

<210> 1

<211> 1008

<212> DNA

<213> Homo sapiens

<220>

<223> Inventor: Ohishi, Takahide; Koizumi, Tomonobu

<220>

<221> CDS

<222> (1).. (1008)

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 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
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ctc atc att gct act aac aca cta gtg gct gtg gct gtg ctg ctg ttg 96
 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 20 25 30

atc cac aag aat gat ggt gtc agt ctc tgc ttc acc ttg aat ctg gct 144
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45

gtg gct gac acc ttg att ggt gtg gcc atc tct ggc cta ctc aca gac 192
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60

cag ctc tcc agc cct tct cgg ccc aca cag aag acc ctg tgc agc ctg 240

Gln	Leu	Ser	Ser	Pro	Ser	Arg	Pro	Thr	Gln	Lys	Thr	Leu	Cys	Ser	Leu	
65					70					75					80	
cgg	atg	gca	ttt	gtc	act	tcc	tcc	gca	gct	gcc	tct	gtc	ctc	acg	gtc	288
Arg	Met	Ala	Phe	Val	Thr	Ser	Ser	Ala	Ala	Ala	Ser	Val	Leu	Thr	Val	
				85					90					95		
atg	ctg	atc	acc	ttt	gac	agg	tac	ctt	gcc	atc	aag	cag	ccc	ttc	cgc	336
Met	Leu	Ile	Thr	Phe	Asp	Arg	Tyr	Leu	Ala	Ile	Lys	Gln	Pro	Phe	Arg	
			100					105					110			
tac	ttg	aag	atc	atg	agt	ggg	ttc	gtg	gcc	ggg	gcc	tgc	att	gcc	ggg	384
Tyr	Leu	Lys	Ile	Met	Ser	Gly	Phe	Val	Ala	Gly	Ala	Cys	Ile	Ala	Gly	
		115					120					125				
ctg	tgg	tta	gtg	tct	tac	ctc	att	ggc	ttc	ctc	cca	ctc	gga	atc	ccc	432
Leu	Trp	Leu	Val	Ser	Tyr	Leu	Ile	Gly	Phe	Leu	Pro	Leu	Gly	Ile	Pro	
	130					135					140					
atg	ttc	cag	cag	act	gcc	tac	aaa	ggg	cag	tgc	agc	ttc	ttt	gct	gta	480
Met	Phe	Gln	Gln	Thr	Ala	Tyr	Lys	Gly	Gln	Cys	Ser	Phe	Phe	Ala	Val	
145					150					155					160	
ttt	cac	cct	cac	ttc	gtg	ctg	acc	ctc	tcc	tgc	gtt	ggc	ttc	ttc	cca	528
Phe	His	Pro	His	Phe	Val	Leu	Thr	Leu	Ser	Cys	Val	Gly	Phe	Phe	Pro	
				165					170					175		
gcc	atg	ctc	ctc	ttt	gtc	ttc	ttc	tac	tgc	gac	atg	ctc	aag	att	gcc	576
Ala	Met	Leu	Leu	Phe	Val	Phe	Phe	Tyr	Cys	Asp	Met	Leu	Lys	Ile	Ala	
			180					185					190			
tcc	atg	cac	agc	cag	cag	att	cga	aag	atg	gaa	cat	gca	gga	gcc	atg	624
Ser	Met	His	Ser	Gln	Gln	Ile	Arg	Lys	Met	Glu	His	Ala	Gly	Ala	Met	
		195					200					205				
gct	gga	ggt	tat	cga	tcc	cca	cgg	act	ccc	agc	gac	ttc	aaa	gct	ctc	672
Ala	Gly	Gly	Tyr	Arg	Ser	Pro	Arg	Thr	Pro	Ser	Asp	Phe	Lys	Ala	Leu	
	210					215					220					
cgt	act	gtg	tct	gtt	ctc	att	ggg	agc	ttt	gct	cta	tcc	tgg	acc	ccc	720
Arg	Thr	Val	Ser	Val	Leu	Ile	Gly	Ser	Phe	Ala	Leu	Ser	Trp	Thr	Pro	
225					230				235					240		
ttc	ctt	atc	act	ggc	att	gtg	cag	gtg	gcc	tgc	cag	gag	tgt	cac	ctc	768
Phe	Leu	Ile	Thr	Gly	Ile	Val	Gln	Val	Ala	Cys	Gln	Glu	Cys	His	Leu	
				245				250					255			

tac cta gtg ctg gaa cgg tac ctg tgg ctg ctc ggc gtg ggc aac tcc 816
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270

ctg ctc aac cca ctc atc tat gcc tat tgg cag aag gag gtg cga ctg 864
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285

cag ctc tac cac atg gcc cta gga gtg aag aag gtg ctc acc tca ttc 912
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300

ctc ctc ttt ctc tcg gcc agg aat tgt ggc cca gag agg ccc agg gaa 960
 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320

agt tcc tgt cac atc gtc act atc tcc agc tca gag ttt gat ggc taa 1008
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 325 330 335

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 <212> PRT
 <213> Homo sapiens

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 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
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 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 100 105 110
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140

Met	Phe	Gln	Gln	Thr	Ala	Tyr	Lys	Gly	Gln	Cys	Ser	Phe	Phe	Ala	Val
145					150					155					160
Phe	His	Pro	His	Phe	Val	Leu	Thr	Leu	Ser	Cys	Val	Gly	Phe	Phe	Pro
				165					170						175
Ala	Met	Leu	Leu	Phe	Val	Phe	Phe	Tyr	Cys	Asp	Met	Leu	Lys	Ile	Ala
				180				185					190		
Ser	Met	His	Ser	Gln	Gln	Ile	Arg	Lys	Met	Glu	His	Ala	Gly	Ala	Met
		195					200					205			
Ala	Gly	Gly	Tyr	Arg	Ser	Pro	Arg	Thr	Pro	Ser	Asp	Phe	Lys	Ala	Leu
	210					215					220				
Arg	Thr	Val	Ser	Val	Leu	Ile	Gly	Ser	Phe	Ala	Leu	Ser	Trp	Thr	Pro
225					230					235					240
Phe	Leu	Ile	Thr	Gly	Ile	Val	Gln	Val	Ala	Cys	Gln	Glu	Cys	His	Leu
				245					250					255	
Tyr	Leu	Val	Leu	Glu	Arg	Tyr	Leu	Trp	Leu	Leu	Gly	Val	Gly	Asn	Ser
			260				265						270		
Leu	Leu	Asn	Pro	Leu	Ile	Tyr	Ala	Tyr	Trp	Gln	Lys	Glu	Val	Arg	Leu
		275					280					285			
Gln	Leu	Tyr	His	Met	Ala	Leu	Gly	Val	Lys	Lys	Val	Leu	Thr	Ser	Phe
		290				295					300				
Leu	Leu	Phe	Leu	Ser	Ala	Arg	Asn	Cys	Gly	Pro	Glu	Arg	Pro	Arg	Glu
305					310					315					320
Ser	Ser	Cys	His	Ile	Val	Thr	Ile	Ser	Ser	Ser	Glu	Phe	Asp	Gly	
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<210> 3
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 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1)..(1008)

<400> 3																
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Met	Glu	Ser	Ser	Phe	Ser	Phe	Gly	Val	Ile	Leu	Ala	Val	Leu	Thr	Ile	
1				5				10					15			
ctt	atc	att	gct	gtt	aat	gcg	ctg	gtg	gtt	gtg	gct	atg	ctg	cta	tca	96
Leu	Ile	Ile	Ala	Val	Asn	Ala	Leu	Val	Val	Val	Ala	Met	Leu	Leu	Ser	
			20					25					30			
atc	tac	aag	aat	gat	ggt	gtt	ggc	ctt	tgc	ttc	acc	tta	aat	ctg	gcc	144
Ile	Tyr	Lys	Asn	Asp	Gly	Val	Gly	Leu	Cys	Phe	Thr	Leu	Asn	Leu	Ala	

35	40	45	
gtg gct gat acc ttg att ggc	gtg gct att tct ggg	cta gtt aca gac	192
Val Ala Asp Thr Leu Ile Gly	Val Ala Ile Ser Gly	Leu Val Thr Asp	
50	55	60	
cag ctc tcc agc tct gct cag cac	aca cag aag acc ttg tgt agc ctt		240
Gln Leu Ser Ser Ser Ala Gln His Thr	Gln Lys Thr Leu Cys Ser Leu		
65	70	75	80
cgg atg gca ttc gtc act tct tct	gca gcc gcc tct gtc ctc acg gtc		288
Arg Met Ala Phe Val Thr Ser Ser	Ala Ala Ala Ser Val Leu Thr Val		
85	90	95	
atg ctg att gcc ttt gac agg tac	ctg gcc att aag cag ccc ctc cgt		336
Met Leu Ile Ala Phe Asp Arg Tyr	Leu Ala Ile Lys Gln Pro Leu Arg		
100	105	110	
tac ttc cag atc atg aat ggg ctt	gta gcc gga gga tgc att gca ggg		384
Tyr Phe Gln Ile Met Asn Gly Leu	Val Ala Gly Gly Cys Ile Ala Gly		
115	120	125	
ctg tgg ttg ata tct tac ctt atc	ggc ttc ctc cca ctt gga gtc tcc		432
Leu Trp Leu Ile Ser Tyr Leu Ile	Gly Phe Leu Pro Leu Gly Val Ser		
130	135	140	
ata ttc cag cag acc acc tac cat	ggg ccc tgc acc ttc ttt gct gtg		480
Ile Phe Gln Gln Thr Thr Tyr His	Gly Pro Cys Thr Phe Phe Ala Val		
145	150	155	160
ttt cac cca agg ttt gtg ctg acc	ctc tcc tgt gct ggc ttc ttc cca		528
Phe His Pro Arg Phe Val Leu Thr	Leu Ser Cys Ala Gly Phe Phe Pro		
165	170	175	
gct gtg ctc ctc ttt gtc ttc ttc	tac tgt gac atg ctc aag att gcc		576
Ala Val Leu Leu Phe Val Phe Phe	Tyr Cys Asp Met Leu Lys Ile Ala		
180	185	190	
tct gtg cac agc cag cac atc cgg	aag atg gaa cat gca gga gcc atg		624
Ser Val His Ser Gln His Ile Arg	Lys Met Glu His Ala Gly Ala Met		
195	200	205	
gtt gga gct tgc cgg ccc cca cgg	cct gtc aat gac ttc aag gct gtc		672
Val Gly Ala Cys Arg Pro Pro Arg	Pro Val Asn Asp Phe Lys Ala Val		
210	215	220	

cgg act gta tct gtc ctt att ggg agc ttc acc ctg tcc tgg tot ccg 720
Arg Thr Val Ser Val Leu Ile Gly Ser Phe Thr Leu Ser Trp Ser Pro
225 230 235 240

ttt ctc atc act agc att gtg cag gtg gcc tgc cac aaa tgc tgc ctc 768
Phe Leu Ile Thr Ser Ile Val Gln Val Ala Cys His Lys Cys Cys Leu
245 250 255

tac caa gtg ctg gaa aaa tac ctc tgg ctc ctt gga gtt ggc aac tcc 816
Tyr Gln Val Leu Glu Lys Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260 265 270

ctg ctc aac cca ctc atc tat gcc tat tgg cag agg gag gtt cgg cag 864
Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Arg Glu Val Arg Gln
275 280 285

cag ctc tgc cac atg gcc ctg ggg gtg aag aag ttc ttt act tca atc 912
Gln Leu Cys His Met Ala Leu Gly Val Lys Lys Phe Phe Thr Ser Ile
290 295 300

ttc ctc ctt ctc tcg gcc agg aat cgt ggt cca cag agg acc cga gaa 960
Phe Leu Leu Leu Ser Ala Arg Asn Arg Gly Pro Gln Arg Thr Arg Glu
305 310 315 320

agc tcc tat cac atc gtc act atc agc cag ccg gag ctc gat ggc tag 1008
Ser Ser Tyr His Ile Val Thr Ile Ser Gln Pro Glu Leu Asp Gly
325 330 335

<210> 4

<211> 335

<212> PRT

<213> Rattus sp.

<400> 4

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Thr Ile
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Leu Ile Ile Ala Val Asn Ala Leu Val Val Val Ala Met Leu Leu Ser
20 25 30

Ile Tyr Lys Asn Asp Gly Val Gly Leu Cys Phe Thr Leu Asn Leu Ala
35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Val Thr Asp
50 55 60

Gln Leu Ser Ser Ser Ala Gln His Thr Gln Lys Thr Leu Cys Ser Leu
65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val

85								90								95							
Met	Leu	Ile	Ala	Phe	Asp	Arg	Tyr	Leu	Ala	Ile	Lys	Gln	Pro	Leu	Arg								
100								105								110							
Tyr	Phe	Gln	Ile	Met	Asn	Gly	Leu	Val	Ala	Gly	Gly	Cys	Ile	Ala	Gly								
115								120								125							
Leu	Trp	Leu	Ile	Ser	Tyr	Leu	Ile	Gly	Phe	Leu	Pro	Leu	Gly	Val	Ser								
130								135								140							
Ile	Phe	Gln	Gln	Thr	Thr	Tyr	His	Gly	Pro	Cys	Thr	Phe	Phe	Ala	Val								
145								150								155							
Phe	His	Pro	Arg	Phe	Val	Leu	Thr	Leu	Ser	Cys	Ala	Gly	Phe	Phe	Pro								
165								170								175							
Ala	Val	Leu	Leu	Phe	Val	Phe	Phe	Tyr	Cys	Asp	Met	Leu	Lys	Ile	Ala								
180								185								190							
Ser	Val	His	Ser	Gln	His	Ile	Arg	Lys	Met	Glu	His	Ala	Gly	Ala	Met								
195								200								205							
Val	Gly	Ala	Cys	Arg	Pro	Pro	Arg	Pro	Val	Asn	Asp	Phe	Lys	Ala	Val								
210								215								220							
Arg	Thr	Val	Ser	Val	Leu	Ile	Gly	Ser	Phe	Thr	Leu	Ser	Trp	Ser	Pro								
225								230								235							
Phe	Leu	Ile	Thr	Ser	Ile	Val	Gln	Val	Ala	Cys	His	Lys	Cys	Cys	Leu								
245								250								255							
Tyr	Gln	Val	Leu	Glu	Lys	Tyr	Leu	Trp	Leu	Leu	Gly	Val	Gly	Asn	Ser								
260								265								270							
Leu	Leu	Asn	Pro	Leu	Ile	Tyr	Ala	Tyr	Trp	Gln	Arg	Glu	Val	Arg	Gln								
275								280								285							
Gln	Leu	Cys	His	Met	Ala	Leu	Gly	Val	Lys	Lys	Phe	Phe	Thr	Ser	Ile								
290								295								300							
Phe	Leu	Leu	Leu	Ser	Ala	Arg	Asn	Arg	Gly	Pro	Gln	Arg	Thr	Arg	Glu								
305								310								315							
Ser	Ser	Tyr	His	Ile	Val	Thr	Ile	Ser	Gln	Pro	Glu	Leu	Asp	Gly									
325								330								335							

<210>	5
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<212>	DNA
<213>	Artificial Sequence

<220>
<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 5
aaaagcttcc tgcagcctcc agctctcc

<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

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24

<210> 7
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 <212> DNA
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<400> 7
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 taagactcta atgaccgct ggtcctgagg aagaggtgct gacgaccaag gagatcttcc 180
 cacagacca gcaccaggga aatggtccgg aaattgcagc ctcagcccc agcoatctgc 240
 cgaccccccc acccaggcc ctaatgggcc aggcggcagg ggttgacagg taggggagat 300
 gggctctgag actataaagc cagcgggggc ccagcagccc tcagccctcc aggacaggct 360
 gcatcagaag aggccat 377